

Figure 1

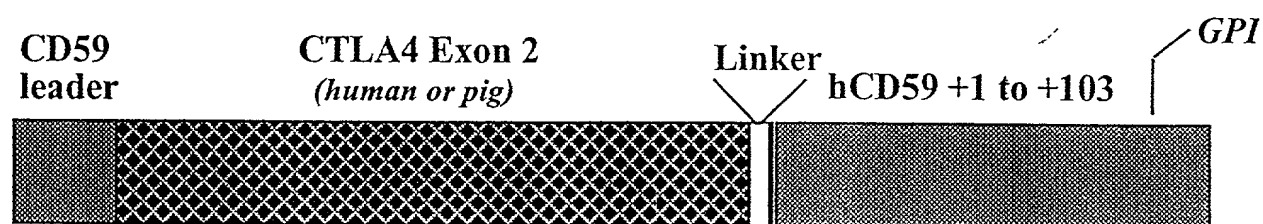


Diagram of Chimeric Molecule

Fig 1

Sequence Range: 1 to 833

```

      10      20      30      40      50
GGATCCTGGGCGCCGCCAGGTTCTGTGGACAATCACAATGGGAATCCAAG
CCTAGGACCCGCGGCGGTCCAAGACACCTGTTAGTGTACCTTAGGTTCC
                                M G I Q>
                                >
                                M G I Q>
                                >

      60      70      80      90     100
GAGGGTCTGTCCTGTTCTGGGCTGCTGCTCGTCCTAGCTGTCTTCTGCCAT
CTCCCAGACAGGACAAGCCCGACGACGAGCAGGATCGACAGAAGACGGTA
G G S V L F G L L L V L A V F C H>
      TRANSLATION OF PIGCCBAM/RIMP [ A] >
G G S V L F G L L L V L A V F C H>
      >

     110     120     130     140     150
TCAGGTCATAGCCTGCATATGCACGTGGCCCAGCCTGCAGTGGTGCTGGC
AGTCCAGTATCGGACGTATACGTGCACCGGGTCGGACGTCACCACGACCG
S G H S L H M H V A Q P A V V L A>
      TRANSLATION OF PIGCCBAM/RIMP [ A] >
S G H S L H M H V A Q P A V V L A>
      >

     160     170     180     190     200
CAACAGCCGGGGTGTGTCAGCTTTGTGTGTGAGTATGGGTCTGCAGGCA
GTTGTCGGCCCCACAACGGTCGAAACACACACTCATACCAGACGTCCGT
N S R G V A S F V C E Y G S A G>
      TRANSLATION OF PIGCCBAM/RIMP [ A] >
N S R G V A S F V C E Y G S A G>
      >

     210     220     230     240     250
AAGCTGCCGAGGTCCGGGTGACAGTGCTGCGGCGGGCCGGCAGCCAGATG
TTCGACGGCTCCAGGCCCCACTGTCACGACGCCGCCCGGGCTCGGTCTAC
K A A E V R V T V L R R A G S Q M>
      TRANSLATION OF PIGCCBAM/RIMP [ A] >
K A A E V R V T V L R R A G S Q M>
      >

     260     270     280     290     300
ACTGAAGTCTGTGCCGCGACATATACTGTGGAGGATGAGTTGACCTTCCT
TGACTTCAGACACGGCGCTGTATATGACACCTCCTACTCAACTGGAAGGA
T E V C A A T Y T V E D E L T F L>
      TRANSLATION OF PIGCCBAM/RIMP [ A] >

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Fig. 2A1

T E V C A A T Y T V E D E L T F L>
>

310 320 330 340 350
TGATGACTCTACATGCACTGGCACCTCCACCGAAAACAAAGTGAACCTCA
ACTACTGAGATGTACGTGACCGTGGAGGTGGCTTTTGTTCACCTGGAGT
D D S T C T G T S T E N K V N L>
TRANSLATION OF PIGCCBAM/RIMP [A]>
D D S T C T G T S T E N K V N L>
>

360 370 380 390 400
CCATCCAAGGGCTGAGAGCCGTGGACACTGGGCTCTACATCTGCAAGGTG
GGTAGGTTCCCGACTCTCGGCACCTGTGACCCGAGATGTAGACGTTCCAC
T I Q G L R A V D T G L Y I C K V>
TRANSLATION OF PIGCCBAM/RIMP [A]>
T I Q G L R A V D T G L Y I C K V>
>

410 420 430 440 450
GAGCTCCTGTACCCACCACCCTACTATGTGGGTATGGGCAACGGGACCCA
CTCGAGGACATGGGTGGTGGGATGATACCCCATACCCGTTGCCCTGGGT
E L L Y P P P Y Y V G M G N G T Q>
TRANSLATION OF PIGCCBAM/RIMP [A]>
E L L Y P P P Y Y V G M G N G T Q>
>

460 470 480 490 500
GATTTATGTCATTGATCCAGAACCATGCCCAGATTCTGATTTCCGGTGGCG
CTAAATACAGTAACTAGGTCTTGGTACGGGTCTAAGACTAAAGCCACCGC
I Y V I D P E P C P D S D F G G>
TRANSLATION OF PIGCCBAM/RIMP [A]>
I Y V I D P E P C P D S D F G G>
>

510 520 530 540 550
GTGGCGGTGGCATGCAGTGCTACAACCTGTCCTAACCCAACTGCTGACTGC
CACCGCCACCGTACGTCACGATGTTGACAGGATTGGGTTGACGACTGACG
G G G G M Q C Y N C P N P T A D C>
TRANSLATION OF PIGCCBAM/RIMP [A]>
G G G G M Q C Y N C P N P T A D C>
>

560 570 580 590 600
AAAACAGCCGTCAATTGTTTCATCTGATTTTGATGCGTGTCTCATTACCAA
TTTTGTGCGGCAGTTAACAAGTAGACTAAACTACGCACAGAGTAATGGTT
K T A V N C S S D F D A C L I T K>

TRANSLATION OF PIGCCBAM/RIMP [A] >
K T A V N C S S D F D A C L I T K>
>

610 620 630 640 650
AGCTGGGTTACAAGTGTATAACAAGTGTGGAAGTTTGAGCATTGCAATT
TCGACCCAATGTTTACATATTGTTTACAACCTTCAAACCTCGTAACGTTAA
A G L Q V Y N K C W K F E H C N>

TRANSLATION OF PIGCCBAM/RIMP [A] >
A G L Q V Y N K C W K F E H C N>
>

660 670 680 690 700
TCAACGACGTCAACAACCCGCTTGAGGGAAAATGAGCTAACGTACTACTGC
AGTTGCTGCAGTGTGGGCGAACTCCCTTTTACTCGATTGCATGATGACG
F N D V T T R L R E N E L T Y Y C>

TRANSLATION OF PIGCCBAM/RIMP [A] >
F N D V T T R L R E N E L T Y Y C>
>

710 720 730 740 750
TGCAAGAAGGACCTGTGTAACTTTAACGAACAGCTTGAAAATGGTGGGAC
ACGTTCTTCCCTGGACACATTGAAATTGCTTGTCGAACCTTTTACCACCCTG
C K K D L C N F N E Q L E N G G T>

TRANSLATION OF PIGCCBAM/RIMP [A] >
C K K D L C N F N E Q L E N G G T>
>

760 770 780 790 800
ATCCTTATCAGAGAAAACAGTTCTTCTGCTGGTGAATCCATTTCTGGCAG
TAGGAATAGTCTCTTTTGTCAAGAAGACGACCACTGAGGTAAAGACCGTC
S L S E K T V L L L V T P F L A>

TRANSLATION OF PIGCCBAM/RIMP [A] >
S L S E K T V L L L V T P F L A>
>

810 820 830
CAGCCTGGAGCCTTCATCCCTAAGTCGGAATTC
GTCGGACCTCGGAAGTAGGGATTACAGCCTTAAG
A A W S L H P *>

TRANSLATION OF P >
A A W S L H P *>
>

Sequence Range: 1 to 262

```
      10      20      30      40      50
MGIQGGSVLFGLLLVLAVFCHSGHSLHMHVAQPAVVLANSRGVASFYCEY

      60      70      80      90     100
GSAGKAAEVRVTVLRRAGSQMTEVCAATYTVEDELTFLLDDSTCTGTSTEN

     110     120     130     140     150
KVNLTIQGLRAVDGTGLYICKVELLYPPPYVGMNGTQIYVIDPEPCTDS

     160     170     180     190     200
DFGGGGGGMQCYNCPNPTADCKTAVNCSSDFDAKLITKAGLQVYNKCWKF

     210     220     230     240     250
EHCNFDVTTTRLRENELTYCCKKDLNCFNEQLENGGTSLSSEKTVLLLVY

     260
PFLAAAWSLHP*
```

-19 2A2

Sequence Range: 1 to 830

```

      10      20      30      40      50
GGATCCTGGGCGCCGCAGGTTCTGTGGACAATCACAATGGGAATCCAAGG
CCTAGGACCCGCGGCGTCCAAGACACCTGTTAGTGTTACCCTTAGGTTCC
                                M G I Q G>
                                _____>

      60      70      80      90     100
AGGGTCTGTCTGTTTCGGGCTGCTGCTCGTCCTGGCTGTCTTCTGCCATT
TCCCAGACAGGACAAGCCCGACGACGAGCAGGACCGACAGAAGACGGTAA
  G S V L F G L L L V L A V F C H>
_____TRANSLATION OF HUCCBAM/RIMP [ A ] _____>

     110     120     130     140     150
CAGGTCATAGCCTGCAGATGCACGTGGCCCAGCCTGCTGTGGTACTGGCC
GTCCAGTATCGGACGTCTACGTGCACCGGGTCGGACGACACCATGACCGG
  S G H S L Q M H V A Q P A V V L A>
_____TRANSLATION OF HUCCBAM/RIMP [ A ] _____>

     160     170     180     190     200
AGCAGCCGAGGCATCGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAA
TCGTCCGGCTCCGTAGCGGTCGAAACACACACTCATACTAGAGGTCCGTT
  S S R G I A S F V C E Y A S P G K>
_____TRANSLATION OF HUCCBAM/RIMP [ A ] _____>

     210     220     230     240     250
AGCCACTGAGGTCCGGGTGACAGTGCTTCGGCAGGCTGACAGCCAGGTGA
TCGGTGACTCCAGGCCCACTGTCACGAAGCCGTCCGACTGTCGGTCCACT
  A T E V R V T V L R Q A D S Q V>
_____TRANSLATION OF HUCCBAM/RIMP [ A ] _____>

     260     270     280     290     300
CTGAAGTCTGTGCGGCAACCTACATGACGGGGAATGAGTTGACCTTCCTA
GACTTCAGACACGCCGTTGGATGTACTGCCCCTTACTCAACTGGAAGGAT
  T E V C A A T Y M T G N E L T F L>
_____TRANSLATION OF HUCCBAM/RIMP [ A ] _____>

     310     320     330     340     350
GATGATTCCATCTGCACGGGCACCTCCAGTGGAAATCAAGTGAACCTCAC
CTACTAAGGTAGACGTGCCCCGTGGAGGTCACCTTTAGTTCACTTGGAGTG
  D D S I C T G T S S G N Q V N L T>
_____TRANSLATION OF HUCCBAM/RIMP [ A ] _____>

     360     370     380     390     400
TATCCAAGGACTGAGGGCCATGGACACGGGACTCTACATCTGCAAGGTGG
ATAGGTTCTGACTCCCGGTACCTGTGCCCTGAGATGTAGACGTTCCACC
```

Fig 2B1

I Q G L R A M D T G L Y I C K V>

TRANSLATION OF HUCCBAM/RIMP [A] >

410 420 430 440 450
AGCTCATGTACCCACCGCCATACTACCTGGGCATAGGCAACGGAACCCAG
TCGAGTACATGGGTGGCGGTATGATGGACCCGTATCCGTTGCCTTGGGTC
E L M Y P P P Y Y L G I G N G T Q>

TRANSLATION OF HUCCBAM/RIMP [A] >

460 470 480 490 500
ATTTATGTAATTGATCCAGAACCGTGCCAGATTCTGACGCCTCCGCCTC
TAAATACATTAAGTCTTGGCACGGGTCTAAGACTGCGGAGGCGGAG
I Y V I D P E P C P D S D A S A S>

TRANSLATION OF HUCCBAM/RIMP [A] >

510 520 530 540 550
CGCCTCCCTGCAGTGCTACAACCTGTCCTAACCCAACTGCTGACTGCAAAA
GCGGAGGGACGTCACGATGTTGACAGGATTGGGTTGACGACTGACGTTTT
A S L Q C Y N C P N P T A D C K>

TRANSLATION OF HUCCBAM/RIMP [A] >

560 570 580 590 600
CAGCCGTCAATTGTTTCATCTGATTTTGATGCGTGTCTCATTACCAAAGCT
GTCGGCAGTTAACAAGTAGACTAAACTACGCACAGAGTAATGGTTTCGA
T A V N C S S D F D A C L I T K A>

TRANSLATION OF HUCCBAM/RIMP [A] >

610 620 630 640 650
GGGTTACAAGTGTTATAACAAGTGTTGGAAGTTTGAGCATTGCAATTTCAA
CCCAATGTTTCACATATTGTTTCACAACCTTCAAACCTCGTAACGTAAAGTT
G L Q V Y N K C W K F E H C N F N>

TRANSLATION OF HUCCBAM/RIMP [A] >

660 670 680 690 700
CGACGTCACAACCCGCTTGAGGGAAAATGAGCTAACGTACTACTGCTGCA
GCTGCAGTGTTGGGCGAACTCCCTTTTACTCGATTGCATGATGACGACGT
D V T T R L R E N E L T Y Y C C>

TRANSLATION OF HUCCBAM/RIMP [A] >

710 720 730 740 750
AGAAGGACCTGTGTAACCTTAAACGAACAGCTTGAAAATGGTGGGACATCC
TCTTCCTGGACACATTGAAATTGCTTGTCGAACTTTTACCACCCTGTAGG
K K D L C N F N E Q L E N G G T S>

TRANSLATION OF HUCCBAM/RIMP [A] >

760 770 780 790 800
TTATCAGAGAAAACAGTTCTTCTGCTGGTGACTCCATTTCTGGCAGCAGC

AATAGTCTCTTTTGTCAAGAAGACGACCACTGAGGTAAAGACCGTCGTCG
L S E K T V L L L V T P F L A A A>
_____TRANSLATION OF HUCCBAM/RIMP [A] _____>

810 820 830
CTGGAGCCTTCATCCCTAAGTCGGAATTCC
GACCTCGGAAGTAGGGATTCAGCCTTAAGG
W S L H P *>
_____TRANSLATION _____>

Sequence Range: 1 to 261

```

      10      20      30      40      50
MGIQGGSVLFGLLLVLAVFCHSGHSLQMHVAQPAVVLAASSRGIASFVCEY

      60      70      80      90     100
ASPGKATEVRVTVLRQADSQVTEVCAATYMTGNELTFLDDSICTGTSSGN

     110     120     130     140     150
QVNLTIQGLRAMDTGLYICKVELMYPPPYLGIGNGTQIYVIDPEPCPDS

     160     170     180     190     200
DASASASLQCYNCPNPTADCKTAVNCSSDFDACLITKAGLQVYNKCWFFE

     210     220     230     240     250
HCNFNDVTTTRLRENELTYCCKKDLCNFNEQLENGGTSLSSEKTVLLLVTP

     260
FLAAAWSLHP*
```

Fig 2B2

Sequence Range: 1 to 672

```

      10      20      30      40      50
ATGGCTCGTTTCGGATTCCGGAGCCATGGGGCTTGGCTGGAGCTTACTTC
TACCGAGCAAAGCCTAAGGCCTCGGTACCCCGAACCGACCTCGAATGAAG
M A R F G F R S H G A W L E L T S>
      TRANSLATION OF PCTLA4SEQ [ A ] _____>

      60      70      80      90     100
TAGGACCTGGCCCTGTACAGCTCTGTTTTCTTCTTCTTCATCCCTGTCT
ATCCTGGACCGGGACATGTGAGACAAAAGAGAAGAGAAGTAGGGACAGA
R T W P C T A L F S L L F I P V>
      TRANSLATION OF PCTLA4SEQ [ A ] _____>

     110     120     130     140     150
TCTCCAAAGGGATGCACGTGGCCCAGCCTGCAGTGGTGCTGGCCAACAGC
AGAGGTTTCCCTACGTGCACCGGGTCGGACGTCACCACGACCGGTTGTCG
F S K G M H V A Q P A V V L A N S>
      TRANSLATION OF PCTLA4SEQ [ A ] _____>

     160     170     180     190     200
CGGGGTGTTGCCAGCTTTGTGTGTGAGTATGGGTCTGCAGGCAAAGCTGC
GCCCCACAACGGTCGAAACACACACTCATACCCAGACGTCGGTTTCGACG
R G V A S F V C E Y G S A G K A A>
      TRANSLATION OF PCTLA4SEQ [ A ] _____>

     210     220     230     240     250
CGAGGTCCGGGTGACAGTGCTGCGGCGGGCCGGCAGCCAGATGACTGAAG
GCTCCAGGCCCACTGTACGACGCCGCCCGGCCGTCGGTCTACTGACTTC
E V R V T V L R R A G S Q M T E>
      TRANSLATION OF PCTLA4SEQ [ A ] _____>

     260     270     280     290     300
TCTGTGCCGCGACATATACTGTGGAGGATGAGTTGACCTTCCTTGATGAC
AGACACGGCGCTGTATATGACACCTCCTACTCAACTGGAAGGAAGTACTG
V C A A T Y T V E D E L T F L D D>
      TRANSLATION OF PCTLA4SEQ [ A ] _____>

     310     320     330     340     350
TCTACATGCACTGGCACCTCCACCGAAAACAAAGTGAACCTCACCATCCA
AGATGTACGTGACCGTGGAGGTGGCTTTTGTTCCTTGGAGTGGTAGGT
S T C T G T S T E N K V N L T I Q>
      TRANSLATION OF PCTLA4SEQ [ A ] _____>

     360     370     380     390     400
AGGGCTGAGAGCCGTGGACACTGGGCTCTACATCTGCAAGGTGGAGCTCC
TCCCGACTCTCGGCACCTGTGACCCGAGATGTAGACGTTCCACCTCGAGG

```

Fig 2c1

G L R A V D T G L Y I C K V E L>

TRANSLATION OF PCTLA4SEQ [A] _____>

410 420 430 440 450
TGTACCCACCACCCTACTATGTGGGTATGGGCAACGGGACCCAGATTTAT
ACATGGGTGGTGGGATGATACACCCATAACCGTTGCCCTGGGTCTAAATA
L Y P P P Y Y V G M G N G T Q I Y>

TRANSLATION OF PCTLA4SEQ [A] _____>

460 470 480 490 500
GTCATTGATCCAGAACCATGCCCAGATTCTGATTTCTGCTCTGGATCCT
CAGTAACTAGGTCTTGGTACGGGTCTAAGACTAAAGGACGAGACCTAGGA
V I D P E P C P D S D F L L W I L>

TRANSLATION OF PCTLA4SEQ [A] _____>

510 520 530 540 550
GGCAACAGTTAGTTCAGGGTTGTTTTTTTACAGCTTCCTCATCACAGCTG
CCGTTGTCAATCAAGTCCCAACAAAAAATGTCGAAGGAGTAGTGTCGAC
A T V S S G L F F Y S F L I T A>

TRANSLATION OF PCTLA4SEQ [A] _____>

560 570 580 590 600
TTTCTTTGAGCAAAATGCTAAAGAAAAGAAGTCCTCTTACTACAGGGGTC
AAAGAACTCGTTTTACGATTTCTTTTCTTCAGGAGAATGATGTCCCCAG
V S L S K M L K K R S P L T T G V>

TRANSLATION OF PCTLA4SEQ [A] _____>

610 620 630 640 650
TATGTGAAAAATGCCCCGACAGAGCCAGAATGTGAAAAGCAATTTTCAGCC
ATACACTTTTTACGGGGCTGTCTCGGTCTTACACTTTTCGTTAAAGTCGG
Y V K N A P T E P E C E K Q F Q P>

TRANSLATION OF PCTLA4SEQ [A] _____>

660 670
TTATTTTATTCCCATCAACTGA
AATAAAATAAGGGTAGTTGACT
Y F I P I N *>

TRANSLATION OF _____>

Sequence Range: 1 to 224

```
      10      20      30      40      50
MACLG FQRHKAQLNLAARTWPCTLLFELLFIPVFECKAMHVAQPAVVLASS

      60      70      80      90     100
RGIASFVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMTGNELTFLDD

     110     120     130     140     150
SICTGTSSGNQVNLTIQGLRAMDTGLYICKVELMYPPPYLGIENGTOIY

     160     170     180     190     200
VIDPEPCPDSDFLWILAAVSSGLFFYSFLLTAVSLSKMLKKRSPLTTGV

     210     220
YVKMPPTPEPECEKQFQPYFIPIN*
```

Fig 2c2 2D2

Sequence Range: 1 to 672

```

      10      20      30      40      50
ATGGCTTGCTTGGATTTCAGCGGCACAAGGCTCAGCTGAACCTGGCTGC
TACCGAACGGAACCTAAAGTCGCCGTGTTCCGAGTCGACTTGGACCGACG
  M  A  C  L  G  F  Q  R  H  K  A  Q  L  N  L  A  A>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

      60      70      80      90     100
CAGGACCTGGCCCTGCACTCTCCTGTTTTTCTTCTCTTCATCCCTGTCT
GTCCTGGACCGGGACGTGAGAGGACAAAAAGAAGAGAAGTAGGGACAGA
  R  T  W  P  C  T  L  L  F  F  L  L  F  I  P  V>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

     110     120     130     140     150
TCTGCAAAGCAATGCACGTGGCCCAGCCTGCTGTGGTACTGGCCAGCAGC
AGACGTTTCGTTACGTGCACCGGGTCGGACGACACCATGACCGGTCGTCG
  F  C  K  A  M  H  V  A  Q  P  A  V  V  L  A  S  S>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

     160     170     180     190     200
CGAGGCATCGCCAGCTTTGTGTGTGAGTATGCATCTCCAGGCAAAGCCAC
GCTCCGTAGCGGTGCGAAACACACACTCATACTAGAGGTCCGTTTCGGTG
  R  G  I  A  S  F  V  C  E  Y  A  S  P  G  K  A  T>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

     210     220     230     240     250
TGAGGTCCGGGTGACAGTGCTTCGGCAGGCTGACAGCCAGGTGACTGAAG
ACTCCAGGCCCACTGTCACGAAGCCGTCCGACTGTCGGTCCACTGACTTC
  E  V  R  V  T  V  L  R  Q  A  D  S  Q  V  T  E>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

     260     270     280     290     300
TCTGTGCGGCAACCTACATGACGGGGAATGAGTTGACCTTCCTAGATGAT
AGACACGCCGTTGGATGTACTGCCCTTACTCAACTGGAAGGATCTACTA
  V  C  A  A  T  Y  M  T  G  N  E  L  T  F  L  D  D>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

     310     320     330     340     350
TCCATCTGCACGGGCACCTCCAGTGGAATCAAGTGAACCTCACTATCCA
AGGTAGACGTGCCCGTGGAGGTCACCTTTAGTTCACTTGGAGTGATAGGT
  S  I  C  T  G  T  S  S  G  N  Q  V  N  L  T  I  Q>
_____TRANSLATION OF HCTLA4SEQ [ A] _____>

     360     370     380     390     400
AGGACTGAGGGCCATGGACACGGGACTCTACATCTGCAAGGTGGAGCTCA
TCCTGACTCCCGGTACCTGTGCCCTGAGATGTAGACGTTCCACCTCGAGT
```

Fig 2D1

G L R A M D T G L Y I C K V E L>

TRANSLATION OF HCTLA4SEQ [A] _____>

410 420 430 440 450
TGTACCCACCGCCATACTACCTGGGCATAGGCAACGGAACCCAGATTTAT
ACATGGGTGGCGGTATGATGGACCCGTATCCGTTGCCTTGGGTCTAAATA
M Y P P P Y Y L G I G N G T Q I Y>

TRANSLATION OF HCTLA4SEQ [A] _____>

460 470 480 490 500
GTAATTGATCCAGAACCGTGCCAGATTCTGACTTCCTCCTCTGGATCCT
CATTAACTAGGTCTTGGCACGGGTCTAAGACTGAAGGAGGAGACCTAGGA
V I D P E P C P D S D F L L W I L>

TRANSLATION OF HCTLA4SEQ [A] _____>

510 520 530 540 550
TGCAGCAGTTAGTTCGGGGTTGTTTTTTTATAGCTTTCTCCTCACAGCTG
ACGTCGTCAATCAAGCCCCAACAAAAAATATCGAAAGAGGAGTGTCGAC
A A V S S G L F F Y S F L L T A>

TRANSLATION OF HCTLA4SEQ [A] _____>

560 570 580 590 600
TTTCTTTTGAGCAAAATGCTAAAGAAAAGAAGCCCTCTTACAACAGGGGTC
AAAGAAACTCGTTTTACGATTTCTTTTCTTCGGGAGAATGTTGTCCCCAG
V S L S K M L K K R S P L T T G V>

TRANSLATION OF HCTLA4SEQ [A] _____>

610 620 630 640 650
TATGTGAAAATGCCCCAACAGAGCCAGAATGTGAAAAGCAATTTTCAGCC
ATACACTTTTACGGGGGTTGTCTCGGTCTTACACTTTTCGTTAAAGTCGG
Y V K M P P T E P E C E K Q F Q P>

TRANSLATION OF HCTLA4SEQ [A] _____>

660 670
TTATTTTATTCCCATCAATTGA
AATAAAATAAGGGTAGTTAACT
Y F I P I N *>

TRANSLATION OF _____>

Sequence Range: 1 to 224

```

      10      20      30      40      50
MARFGFRSHGAWLELTSRTWPCTALFSLLEIPVFSGMHVAQPAVVLANS

      60      70      80      90     100
RGVASFVCEYGSAGKAAEVRVTVLRRAGSQMTEVCAATYTVEDELTFLLDD

     110     120     130     140     150
STCTGTSTENKVNLTIQGLRAVDTGLYICKVELLYPPPPYYVGMGNGTQII

     160     170     180     190     200
VIDPEPCPDSDFLWILATVSSGLFFYSFLITAVSLSKMLKKRSPLTTGV

     210     220
YVKNAPEPECEKQFPYFIPIN*
```

~~202~~ → 202

Sequence Range: 1 to 476

```

      10      20      30      40      50
GAATTCGGGGGCTGAGCGCAGAAGCGGCTCGAGGCTGGAAGAGGATCCT
CTTAAGGCCCGACTCGCGTCTTCGCCGAGCTCCGACCTTCTCCTAGGA

      60      70      80      90     100
GGGCGCCGCAGGTTCTGTGGACAATCACAATGGGAATCCAAGGAGGGTCT
CCCGCGGCGTCCAAGACACCTGTTAGTGTTACCCTTAGGTTCCCTCCCAGA
      M G I Q G G S>
      _____TRANSLATION OF _____>

     110     120     130     140     150
GTCCTGTTCTGGGCTGCTGCTCGTCCTGGCTGTCTTCTGCCATTCAGGTCA
CAGGACAAGCCCGACGACGAGCAGGACCGACAGAAGACGGTAAGTCCAGT
  V L F G L L L V L A V F C H S G H>
  _____TRANSLATION OF HCD59SEQ [ A ] _____>

     160     170     180     190     200
TAGCCTGCAGTGCTACAACCTGTCCTAACCCAACTGCTGACTGCAAAACAG
ATCGGACGTCACGATGTTGACAGGATTGGGTTGACGACTGACGTTTTTGTC
  S L Q C Y N C P N P T A D C K T>
  _____TRANSLATION OF HCD59SEQ [ A ] _____>

     210     220     230     240     250
CCGTCAATTGTTTCATCTGATTTTGATGCGTGTCTCATTACCAAAGCTGGG
GGCAGTTAACAAGTAGACTAAACTACGCACAGAGTAATGGTTTTCGACCC
A V N C S S D F D A C L I T K A G>
  _____TRANSLATION OF HCD59SEQ [ A ] _____>

     260     270     280     290     300
TTACAAGTGTATAACAAGTGTTGGAAGTTTGAGCATTGCAATTTCAACGA
AATGTTACATATTGTTTACAACCTTCAAACCTCGTAACGTTAAAGTTGCT
  L Q V Y N K C W K F E H C N F N D>
  _____TRANSLATION OF HCD59SEQ [ A ] _____>

     310     320     330     340     350
CGTCACAACCCGCTTGAGGGAAAATGAGCTAACGTACTACTGCTGCAAGA
GCAGTGTTGGGCGAACTCCCTTTTACTCGATTGCATGATGACGACGTTCT
  V T T R L R E N E L T Y Y C C K>
  _____TRANSLATION OF HCD59SEQ [ A ] _____>

     360     370     380     390     400
AGGACCTGTGTAACCTTTAACGAACAGCTTGAAAATGGTGGGACATCCTTA
TCCTGGACACATTGAAATTGCTTGTCGAACTTTTACCACCCTGTAGGAAT
K D L C N F N E Q L E N G G T S L>
  _____TRANSLATION OF HCD59SEQ [ A ] _____>

```

Fig 2E1

410 420 430 440 450
TCAGAGAAAACAGTTCTTCTGCTGGTGACTCCATTTCTGGCAGCAGCCTG
AGTCTCTTTTGTCAAGAAGACGACCACTGAGGTAAAGACCGTCGTCGGAC
S E K T V L L L V T P F L A A A W>
_____TRANSLATION OF HCD59SEQ [A] _____>

460 470
GAGCCTTCATCCCTAAGTCGGAATTC
CTCGGAAGTAGGGATTTCAGCCTTAAG
S L H P *>
_____TRANSLATI _____>

Sequence Range: 1 to 129

| | | | | |
|---|-----|----|----|-----|
| 10 | 20 | 30 | 40 | 50 |
| MGIQGGSVLFGLLLVLA VFC HSGHSLQCYNC PNPTADCKTAVNCSSDFDA | | | | |
| 60 | 70 | 80 | 90 | 100 |
| CLITKAGLQVYNKCWKFEHCNFNDVTTTRLRENELTYYCCKKDL CNFNEQL | | | | |
| 110 | 120 | | | |
| ENGGTSLSEKTVLLLVT PFLAAAWSLHP* | | | | |

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2E2

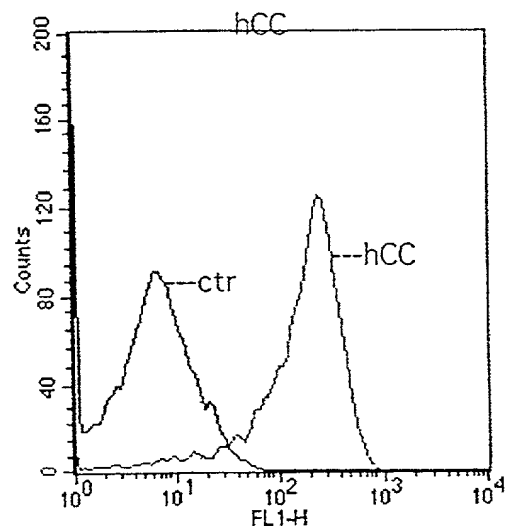
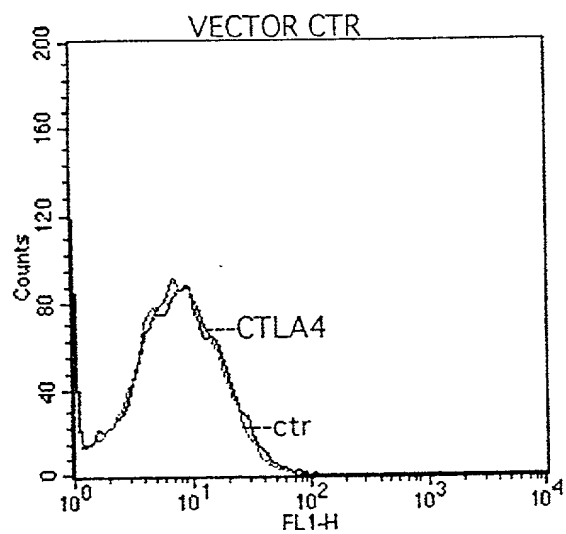


Fig 3

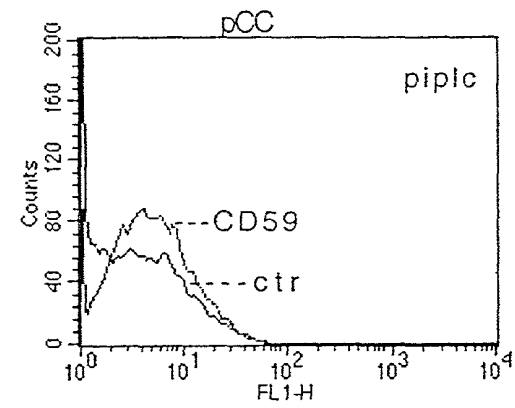
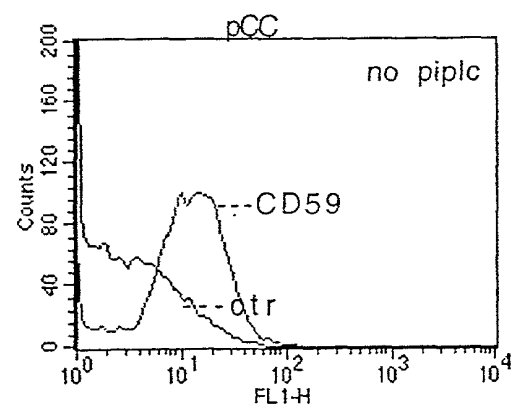
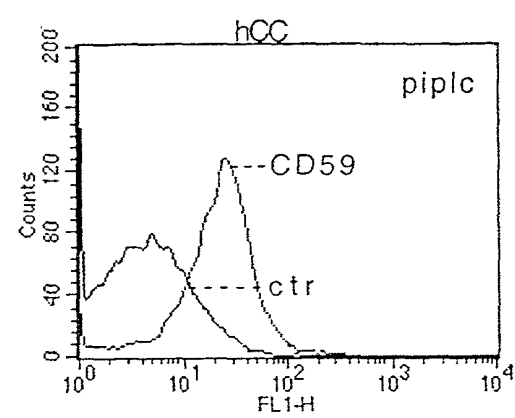
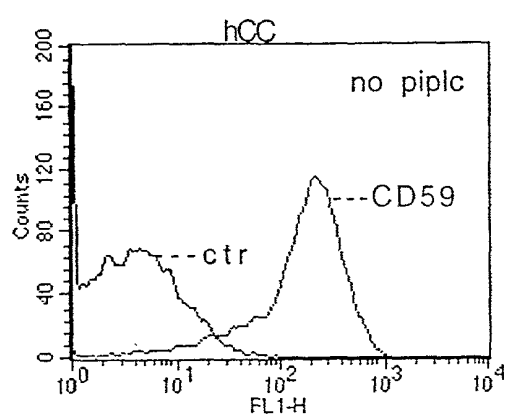
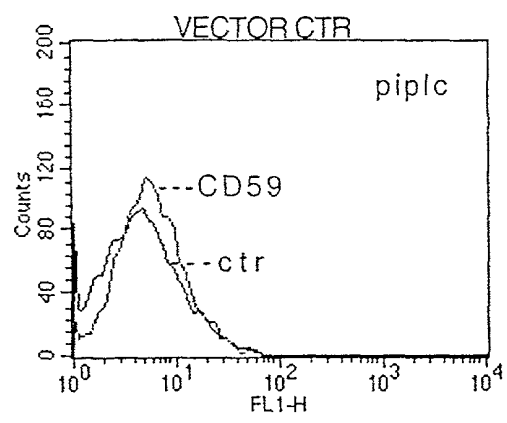
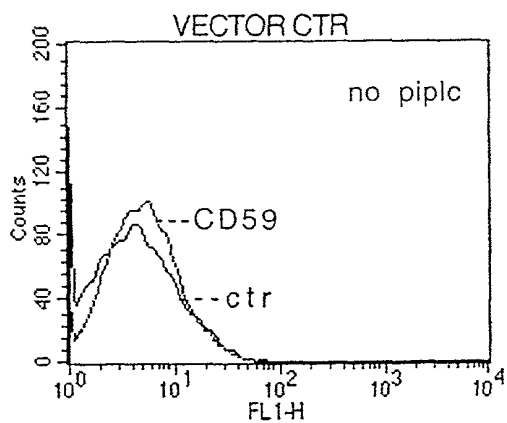


Fig 4

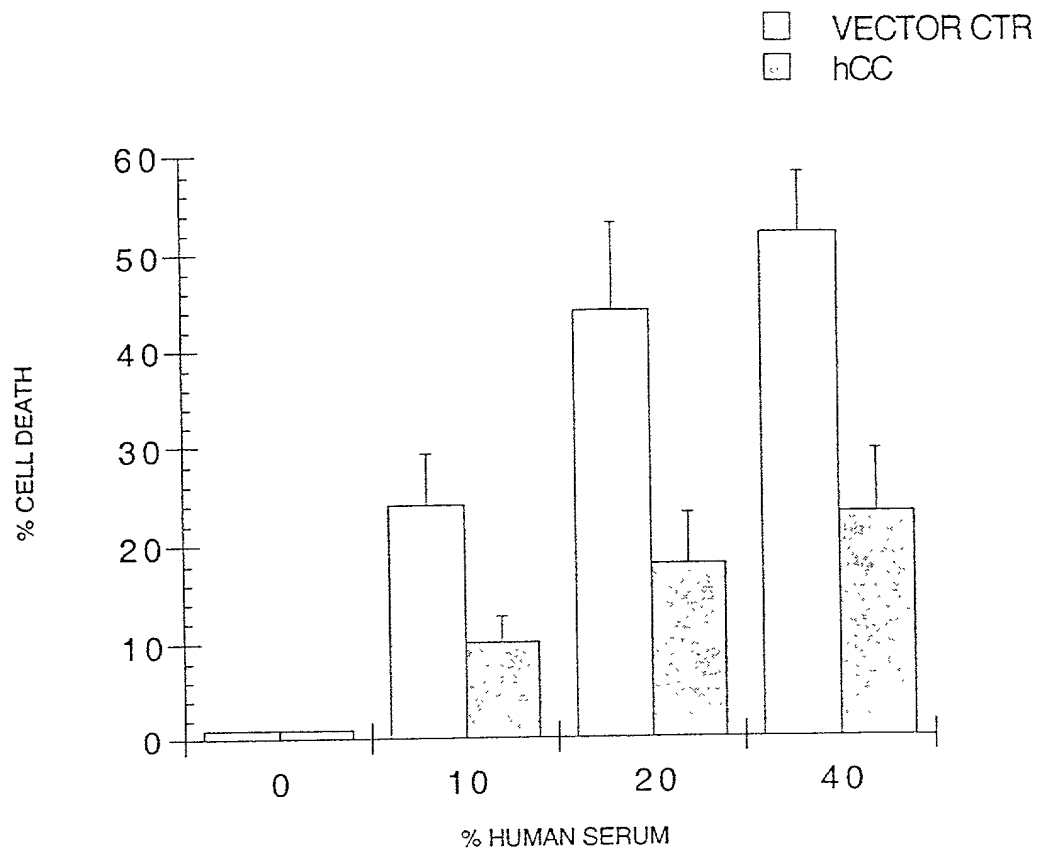


Fig 5

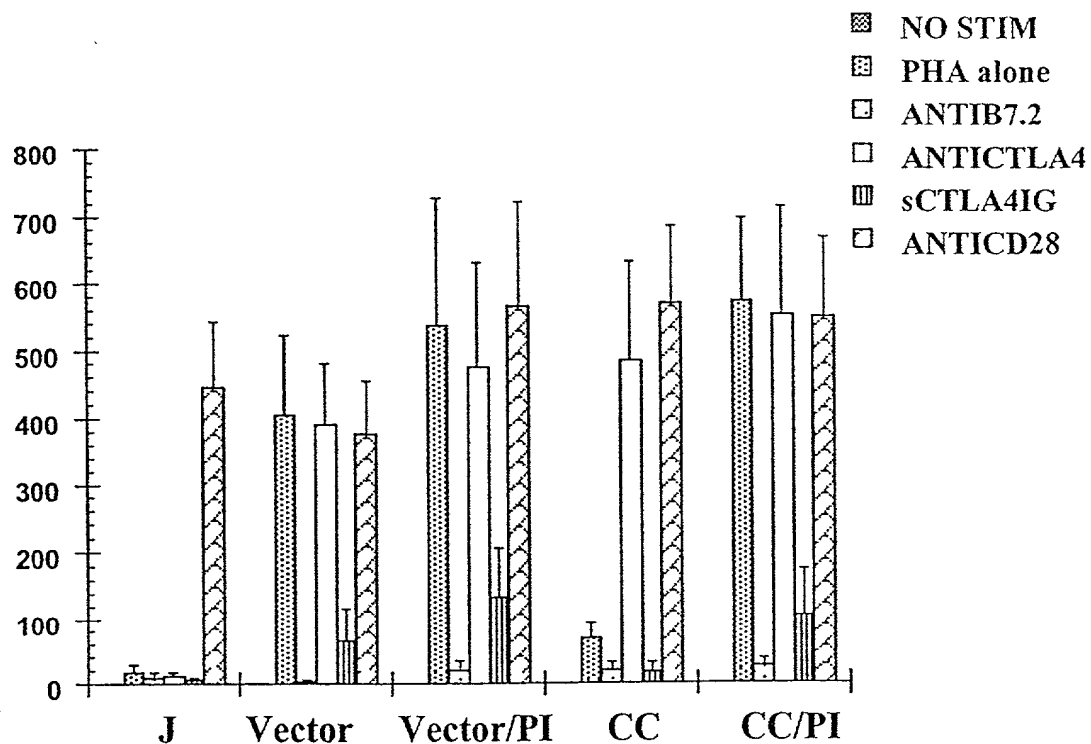


Figure 6 Co-Culture of Jurkat cells with Vector control PAECs or with CC PAECs with and without PI-PLC treatment.

Fig 6

Sequence Range: 1 to 314

10 20 30 40 50
MTVARPSVPAALPLLGELPRLLLLVLLCLPAVWGDCGLPPDVPNAQERLE
60 70 80 90 100
GRTSFPEDTVITYKCEESFVKIPGEKDSVICKLGSQWSDIEEFCNPSCEV
110 120 130 140 150
PTRLNSASLKQPYITQNYFPVGTVEYECPGYRREPSLSPKLTCLDLE
160 170 180 190 200
WSTAVEFCKKKSCPNPGEIRNGQIDVPGGILFGATISFSCNTGKLEFCT
210 220 230 240 250
SSFCLISGSSVQWSDPLPECREIYCPAPPQIDNGIIQGERDHIQYPCCT
260 270 280 290 300
YACNKGFTMIGEHSIYCTVNNDGEWSGPPPECRGKSLTSKVPPTVQKPT
310
TVNVPTTEVSPTSQ

QNLK ✓

FAST ✓

FAST ✓